

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/918:585

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length
Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES)
Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 Use of n's or Xaa's
 (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ✓ Use of <220>
Sequence(s) 157 missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

DATE: 08/10/2001

PATENT APPLICATION: US/09/918,585

TIME: 07:58:44

Input Set : A:\GENENLAW-#94916-v1-Sequence_Listing_as_filed.WPD

Output Set: N:\CRF3\08102001\I918585.raw

Does Not Comply
Corrected Diskette Needed

see page 6 of 8

3 <110> APPLICANT: Ashkenazi, Avi
 4 Baker Kevin P.
 5 Botstein, David
 6 Desnoyers, Luc
 7 Eaton, Dan
 8 Ferrara, Napoleon
 9 Filvaroff, Ellen
 10 Fong, Sherman
 11 Gao, Wei-Qiang
 12 Gerber, Hanspeter
 13 Gerritsen, Mary E.
 14 Goddard, Audrey
 15 Godowski, Paul J.
 16 Grimaldi, J. Christopher
 17 Gurney, Austin L.
 18 Hillan, Kenneth J
 19 Kljavin, Ivar J.
 20 Kuo, Sophia S.
 21 Napier, Mary A.
 22 Pan, James;
 23 Paoni, Nicholas F.
 24 Roy, Margaret Ann
 25 Shelton, David L.
 26 Stewart, Timothy A.
 27 Tumas, Daniel
 28 Williams, P. Mickey
 29 Wood, William I.
 31 <120> TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 32 Acids Encoding the Same
 34 <130> FILE REFERENCE: P2630P1C1
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*improper format
not critical*

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<210> 157
<211> 412
<212> PRT
<213> Artificial

When field 213 is Artificial or Unknown
an explanation is required in fields 220
through fields 223.

<400> 157

Met Gly Leu His Leu Arg Pro Tyr Arg Val Gly Leu Leu Pro Asp
1 5 10 15

Gly Leu Leu Phe Leu Leu Leu Leu Met Leu Leu Ala Asp Pro
20 25 30

Ala Leu Pro Ala Gly Arg His Pro Pro Val Val Leu Val Pro Gly
35 40 45

Asp Leu Gly Asn Gln Leu Glu Ala Lys Leu Asp Lys Pro Thr Val
50 55 60

Val His Tyr Leu Cys Ser Lys Lys Thr Glu Ser Tyr Phe Thr Ile
65 70 75

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VERIFICATION SUMMARY

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Input Set : A:\GENENLAW-#94916-v1-Sequence_Listing_as_filed.WPD

Output Set: N:\CRF3\08102001\I918585.raw

L:36 M:270 C: Current Application Number differs, Replaced Current Application No
L:36 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:241 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:367 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:442 M:256 W: Invalid Numeric Header Field, Wrong Prior FILING DATE:YYYY-MM-DD
L:975 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:977 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:989 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:1009 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:1011 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
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L:1551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30
L:1738 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1740 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
L:1742 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:37
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L:6386 M:258 W: Mandatory Feature missing, <220> FEATURE:
L:6386 M:258 W: Mandatory Feature missing, <223> OTHER INFORMATION: *Errored*
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L:7726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:191
L:8721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:215
L:10650 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10652 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265
L:10654 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:265